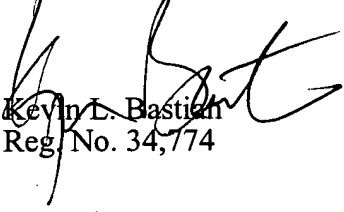


The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy.

Attached hereto is a marked-up version of the changes made to the Specification by the current Amendment. The attached pages are captioned "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**"

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,


Kevin L. Bastian
Reg. No. 34,774

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
San Francisco, California 94111-3834
Tel: (415) 576-0200
Fax: (415) 576-0300
KLB:dmw

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 24 of page 20 has been amended as follows:

Selection of Peptides: The entire amino acid sequence of equine IgE, based on the predicted 566 translated amino acids, was used to generate algorithms to predict accessible epitopes. The algorithms combine the Hopp and Woods hydrophilicity scale, surface probability and accessibility scales, Karplus and Schulz flexibility scale, and Jameson-Wolf antigenic index. Chou and Fasman algorithms were used to determine secondary structure including turns, alpha helices, and beta sheets. Based on data obtained from the above algorithms, six 15 amino acid length peptides were selected for synthesis. The following is a list of the chosen peptides and their location on the epsilon heavy chain: P1 (VTYKRHDLLRTRPRK; SEQ ID NO:1) end portion of C2, P2 (RTRPRKCTESEPRGV; SEQ ID NO:2) end portion of C2, P3 (LAACCKDTKTTNITL; SEQ ID NO:3) beginning of C1, P4 (IQTDQQATTRPKSQW; SEQ ID NO:4) early portion of C4, P5 (LIDGQKVDEQFPQHG; SEQ ID NO:5) middle portion of C2, P6 (RVVASGKWAKQKFTC; SEQ ID NO:6) latter portion of C1. All peptides were manufactured by Sigma Genosys, purified by HPLC, and provided as lyophilized powder.